

gcggccgcccgtacggccATGAAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTGGTT
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CTGGGACTTCAGTGAAGATATCCTGCAAGGCTTCTGGCTACACCTTCACTAACTACTGGC
TAGGTTGGGTAAAGCAGAGGCCTGGACATGGACTTGAGTGGATTGGAGATATTTACCCTG
GAGGTGGTTATACTAACTACAATGAGAAGTTCAAGGGCAAGGCCACACTGACTGCAGACA
CATCCTCCAGCACTGCCTACATGCAGCTCAGTAGCCTGACATCTGAGGACTCTGCTGTCT
ATTTCTGTGCAAGATTTTACTACGGTAGTAGCTACTGGTACTTCGATGTCTGGGGCCAAG
GCACCACGGTCACCGTCTCCTCAGCAAAGACCACTCCTCCGTCTGTTTACCCTCTGGCTC
CTGGTTCTGCGGCTCAGACTAACTCTATGGTGA CTCTGGGATGCCTGGTCAAGGGCTATT
TCCCTGAGCCAGTGACAGTGACCTGGA ACTCTGGATCCCTGTCCAGCGGTGTGCACACCT
TCCCAGCTGTCCTGCAATCTGACCTCTACACTCTGAGCAGCTCAGTGACTGTCCCCTCCA
GCACCTGGCCCAGCGAGACCGTCACCTGCAACGTTGCCACCCGGCTTCTAGCACCAAAG
TTGACAAGAAAATCGTACCGCGCGACTGCTAAccgtagtaagaaaaacttagggtgaaag
ttcatcgggcccgtacggccATGAAACAAAGCACTATTGCACTGGCACTCTTACCGTTAC
TGTTTACCCTGTGACAAAAGCCGACATCGAGCTCACCCAGTCTCCAGCAATCATGGCTG
CATCTGTGGGAGAACTGTCACCATCACATGTGGAGCAAGTGAGAATATTTACGGTGCTT
TAAATTGGTATCAGCGGAAACAGGGAAAATCTCCTCAGCTCCTGATCTATGGTGCAACCA
ACTTGGCAGATGGCATGTCATCGAGGTTCA GTGGCAGTGGATCTGGTAGACAGTATTCTC
TCAAGATCAGTAGCCTGCATCCTGACGATGTTGCAACGTATTACTGTCAAAATGTGTTAA
GTA CTCTCGGACGTTTCGGAGCTGGGACCAAGCTCGAGCTGAAGCGCGCTGATGCTGCAC
CGACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCG
TGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCA
GTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCT
ACAGCATGAGCAGCACCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATA
CCTGTGAGGCCACTCACAAGACATCAACTTACCCATTGTCAAGAGCTTCAACAGGAATG
AGTGTTAGtccgtagtaagaaaaacttagggtgaaagttcatcgggccc

FIG. 1

SYN80 F1:	CGGAATTCGGGGCCCGCTACGGCCATGAAAAGACAGCTATCGCGATTGCAGTGGCACTGGCTGGTT	(SEQ ID NO:12)
SYN80 F2:	TGCAGTGGCACTGGCTGGTTTCGCTACCGTAGCGGAGGCCGAAGTTAACTGCATGAGTCAGGCGCTGGG	(SEQ ID NO:13)
SYN80 F3:	TGCATGAGTCAGGGCCCTGGCTGGTAAGCCCTGGGACTTCAGTGAAGATATCCTGCAAGGCTTCTGGCTA	(SEQ ID NO:14)
SYN80 F4:	ACTGCAGACACATCCTCCAGCACTGCCATGAGCTGAGCTAGTGCCTGACATCTGAGGAC	(SEQ ID NO:15)
SYN80 F5:	GTAGCCTGACATCTGAGGACTCTGCTGTCTATTTCTGTGCAAGATTTTACTACGGTAGTA	(SEQ ID NO:16)
SYN80 F6:	AAGATTTTACTACGGTAGTAGTACTGTGTACTTCGATGTCTGGGGCCCAAGGCACCCACGGT	(SEQ ID NO:17)
SYN80 F7:	CGGGATCCCTGTCCAGCGGTGTGCACACCTTCCAGGTGTCTGCAATCTGACCTCTACA	(SEQ ID NO:18)
SYN80 F8:	CCTGCAATCTGACCTCTACACTCTGAGCAGCTCAGTGAATGTCCCTCCAGCACCTGGCCAGCGAGACC	(SEQ ID NO:19)
SYN80 F9:	GCACCTGGCCCGAGGAGACCGTCACTGCAACGTTGCCACCCGGCTCTAGCACCAAGTTGACAAGAA	(SEQ ID NO:20)
SYN80 F10:	GCCGACATCGAGCTACCCAGTCTCCAGCAATCATGGCTGCATCTGTGGAGAAACTGTACCATCACAT	(SEQ ID NO:21)
SYN80 F11:	AGAAACTGTCACCATCACATGTGGAGCAAGTGAATATTTACGGTCTTTAAATGGTATCAGCGGAAA	(SEQ ID NO:22)
SYN80 F12:	TAAATTTGGTATCAGCGGAAACAGGGAAATCTCTCAGCTCCTGATCTATGGTGCAACCACTTGGCAGA	(SEQ ID NO:23)
SYN80 F13:	ACCGCTCGAGCTGAAGCGCGTGTGTCACCGACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAAC	(SEQ ID NO:24)
SYN80 F14:	CCATCCAGTGAGCAGTTAACTCTGGAGGTGGCTCAGTCGTGTCTTCTTGAACAACCTTACCCCAAG	(SEQ ID NO:25)
SYN80 F15:	GAACAACCTTCTACCCCAAGACATCAATGTCAAGTGAAGATTGATGGCAGTGAACGACAAAATGGCGTC	(SEQ ID NO:26)
SYN80 R1:	CAAGAGCTTCAACAGGAATGAGTGTAGTCCGTAGTAGAAGAACTTAGGGTGAAGTTTCATCGGCCGCAAGCTTGGG	(SEQ ID NO:27)
SYN80 R2:	TGAACGACATAACAGCTATACCTGTGAGGCCACTCAAGACATCAACTTCAAGAGCTTCAACAGGAATG	(SEQ ID NO:28)
SYN80 R3:	GACAGCACCTACAGCATGAGCAGCACCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATA	(SEQ ID NO:29)
SYN80 R4:	GTGAACGACAAAATGGCGTCTGAACAGTTGAGTGTGAGCTGAGGACAGCAAGACAGCACATGAG	(SEQ ID NO:30)
SYN80 R5:	TTACTGTCAAAATGTGTTAAGTACTCTCGGAGCTTCGGAGCTGGGACCAAGCTCGAGCGGAAGCTTGGG	(SEQ ID NO:31)
SYN80 R6:	ATCTGGTAGACAGTATCTCTCAAGATCAGTAGCCTGCATCCTGACGATGTTGCAACGTATTACTGTCAAAATGTGTTAA	(SEQ ID NO:32)
SYN80 R7:	GGTGCAACCAACTTGGCAGATGGCATGTCAATCGAGGTTCAAGTGGCAGTGGATCTGGTAGACAGTATTCTC	(SEQ ID NO:33)
SYN80 R8:	GCACTATTGCACCTGGCACTCTTACCGTTACTGTTTACCCCTGTGACAAAAGCCGACATCGAGCTCACCCCA	(SEQ ID NO:34)
SYN80 R9:	AGAAAACCTTAGGGTGAAGTTTCATCGGGCCGTACGGCCATGAAACAAAGCACTATTGCACTGGCACTC	(SEQ ID NO:35)
SYN80 R10:	AGCACCAAGTTGACAAGAAAATCGTACCGCGGACTGTAAACCGTAGTAAGAAAACCTTAGGGTGAAG	(SEQ ID NO:36)
SYN80 R11:	TGACTCTGGATGCCCTGTCAAGGCTATTTCCCTGAGCCAGTGACAGTGAACCTCTGGATCCCG	(SEQ ID NO:37)
SYN80 R12:	GTCTGTTTACCCCTCTGGCTCTGGTCTGCGGCTCAGACTAACTCTATGGTGAATCTGGATGCCCTGGTC	(SEQ ID NO:38)
SYN80 R13:	TGGGGCCAAGGCACCCAGTCAACCGTCTCTCAGCAAGAACCACTCTCCGTCTGTTTACCCCTCTGGCTC	(SEQ ID NO:39)
SYN80 R14:	GAGGTGGTTATACTAACTACATGAGAATGAAAGTTCAAGGGCAAGGCCACACTGACTGCAGACACATCCTCCAG	(SEQ ID NO:40)
SYN80 R15:	AAAGCAGAGGCCCTGGACATGGACTTGAATGGATGAGATATTTACCCCTGGAGGTGGTTTACTAATACTAC	(SEQ ID NO:41)
SYN80 R16:	TCCTGCAAGGCTTCTGGCTACACCTTCACTAATACTACTGGCTAGGTTGGGTAAAGCAGAGGCCCTGGACATG	(SEQ ID NO:42)

FIG. 2

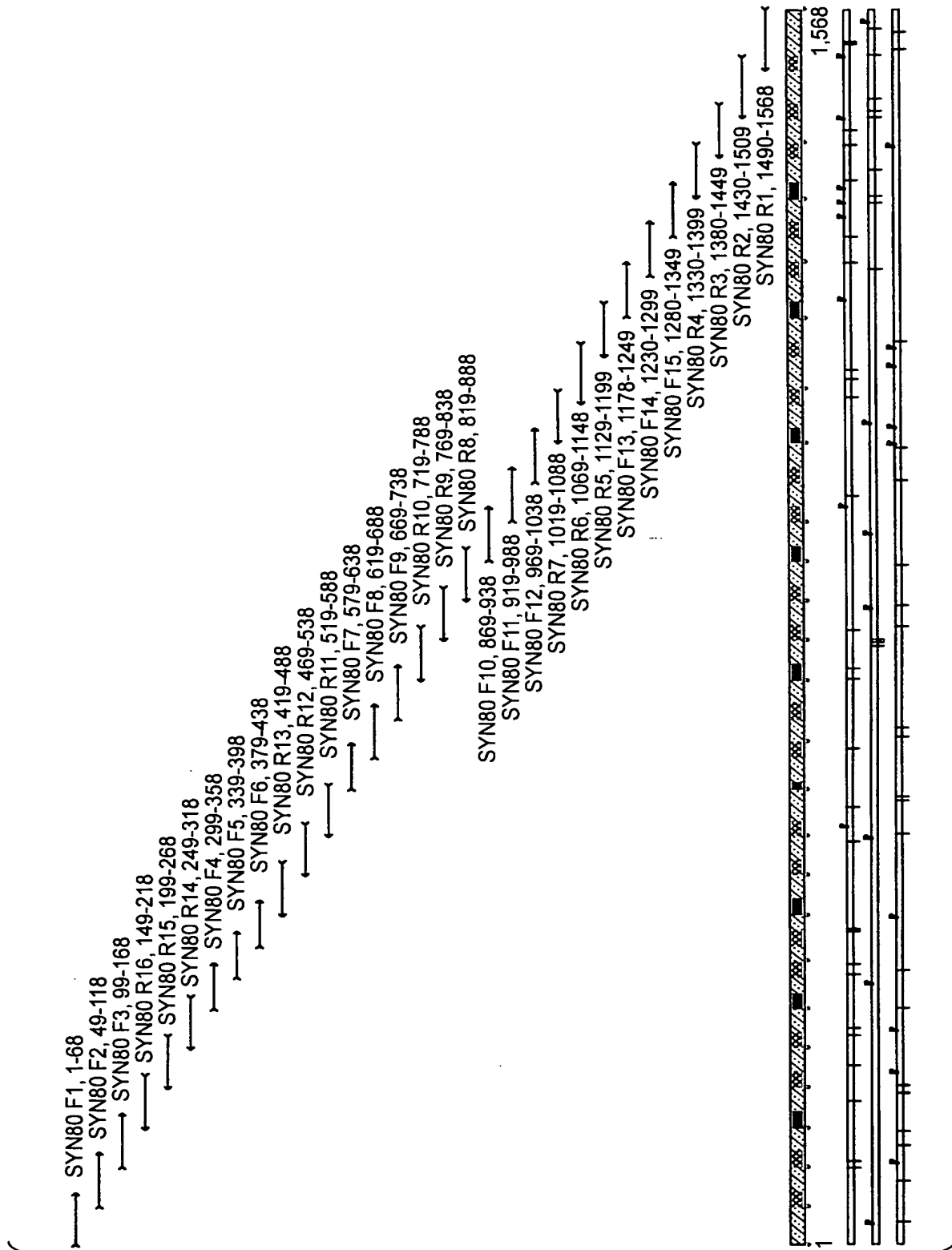
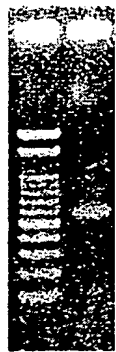


FIG. 3

A



B



FIG. 4

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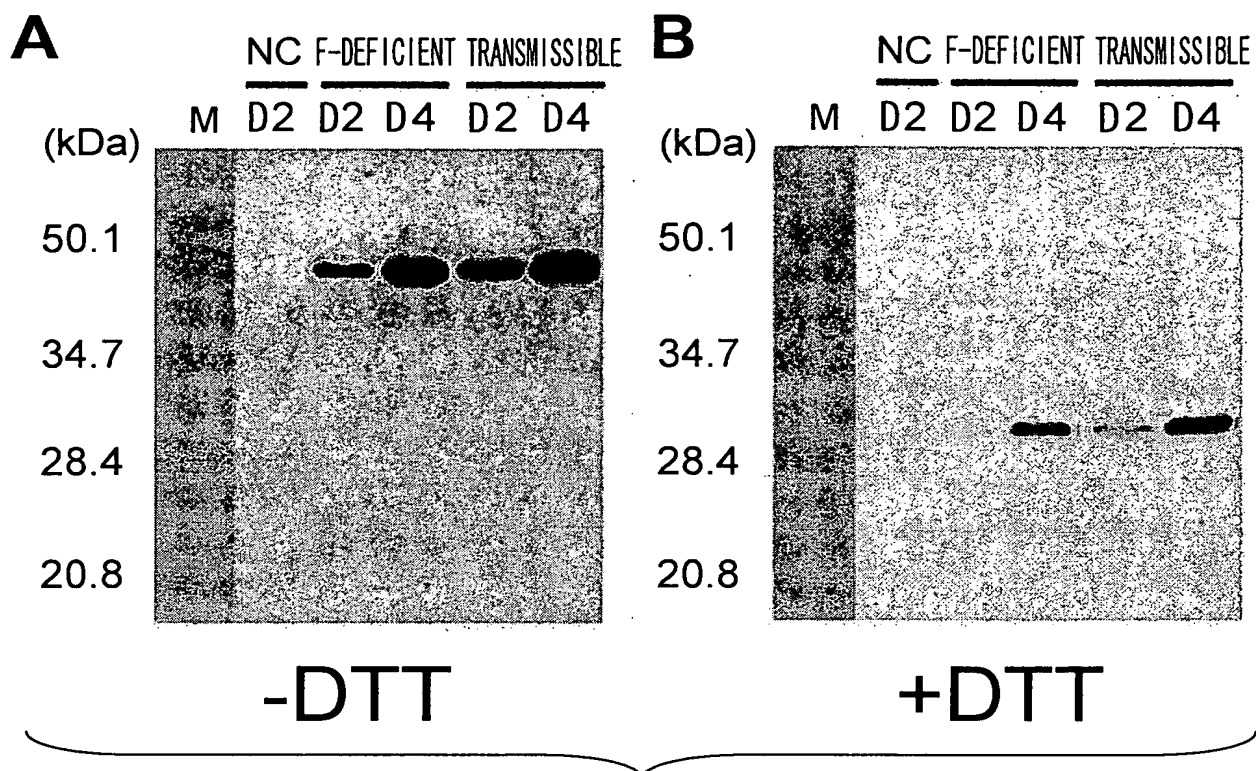
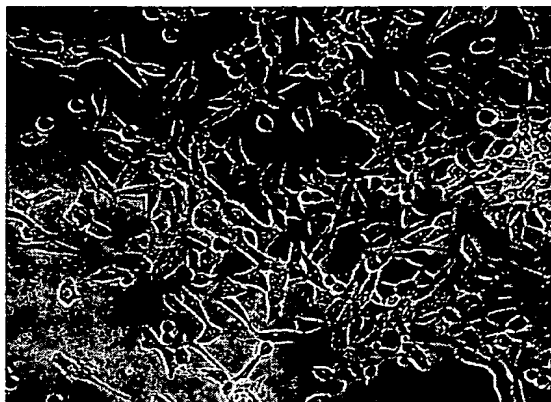


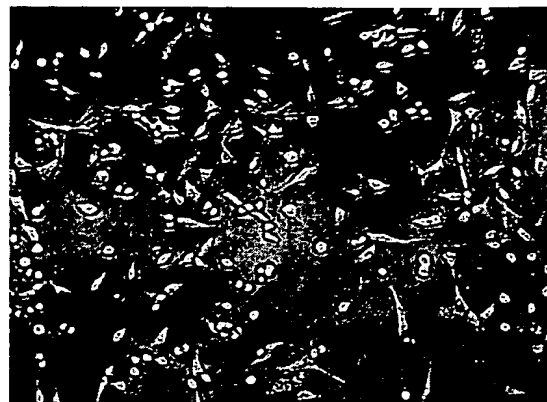
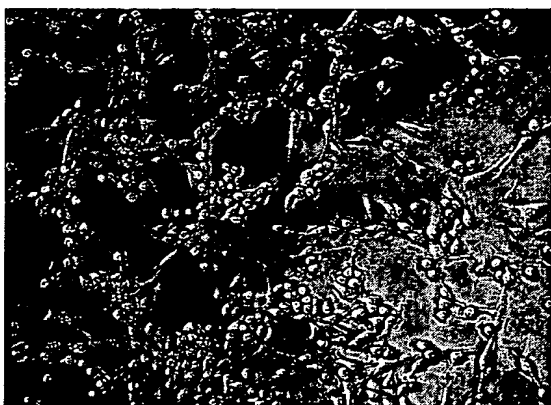
FIG. 5

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(A) — q-pool



(B) + q-pool

(C) + q-pool: SeV¹⁸+GFP

(D)

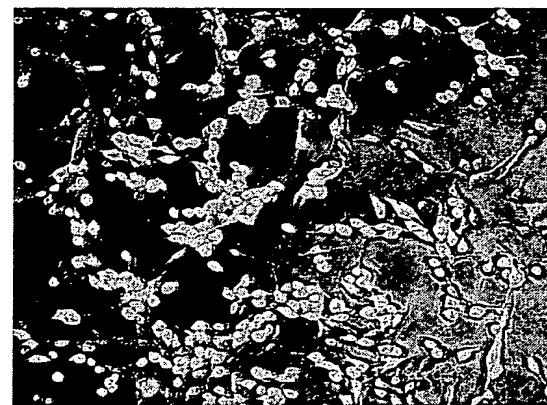
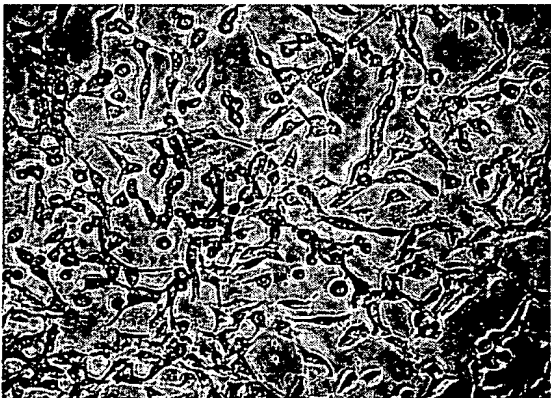
(E) + q-pool: SeV¹⁸+IN-1

FIG. 6

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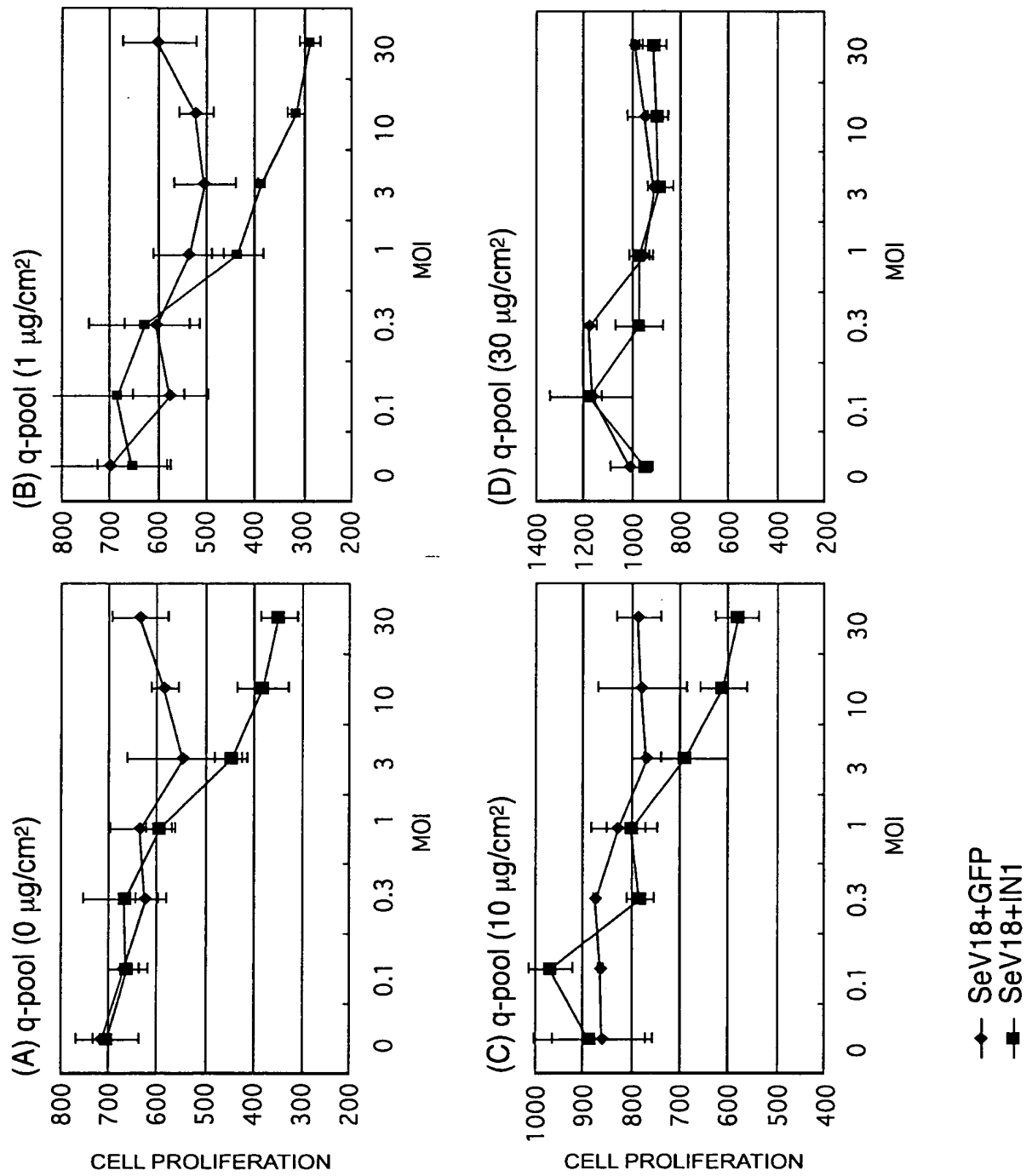
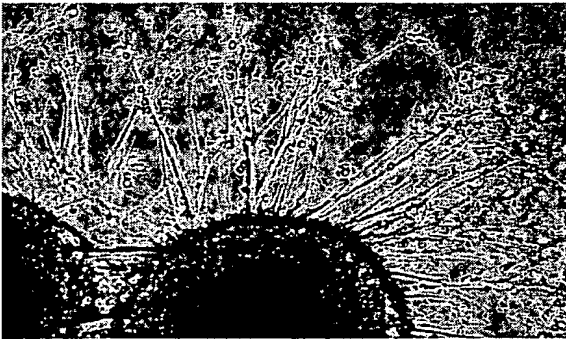
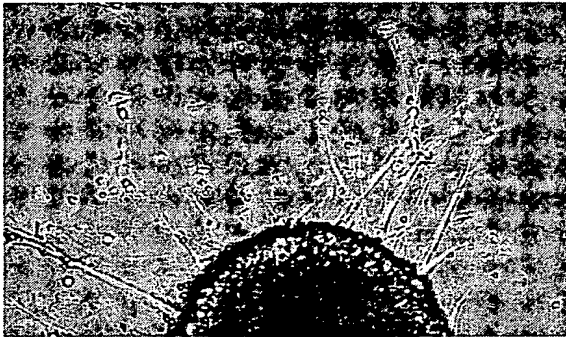
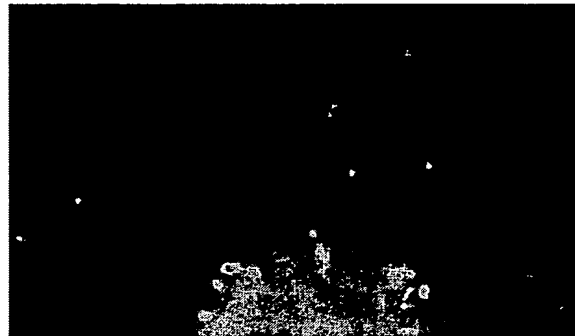
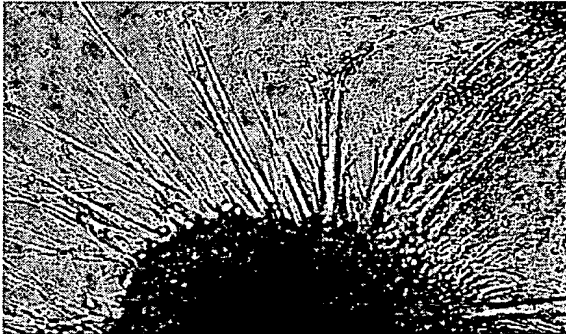
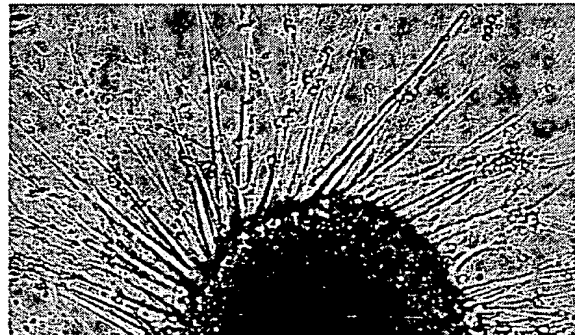


FIG. 7

(A) - q-pool (SeV¹⁸+GFP)**(B)****(C) + q-pool (SeV¹⁸+GFP)****(D)****(E) + q-pool (SeV¹⁸+IN-1) -1****(F) + q-pool (SeV¹⁸+IN-1) -2****FIG. 8**

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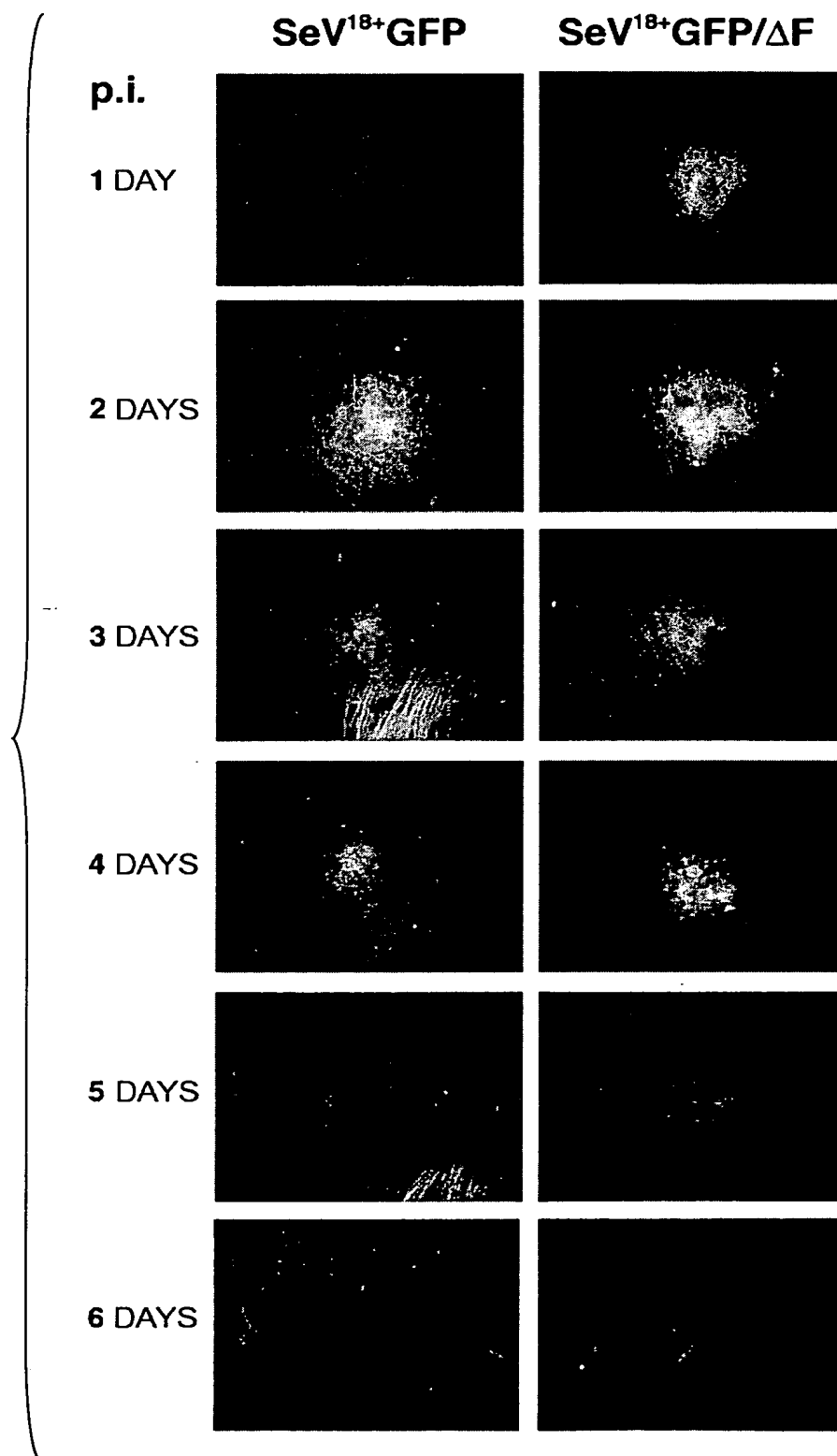


FIG. 9

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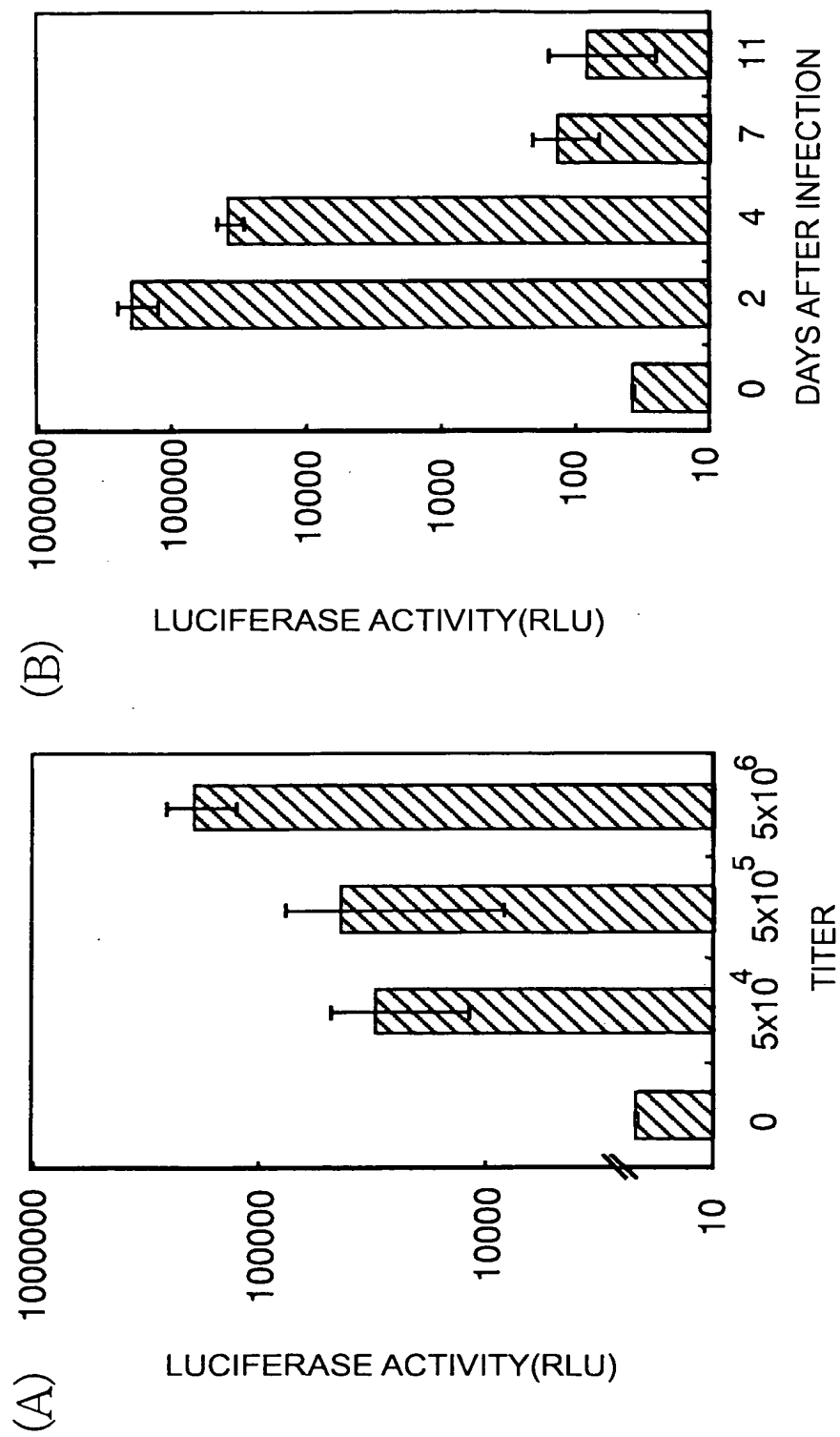
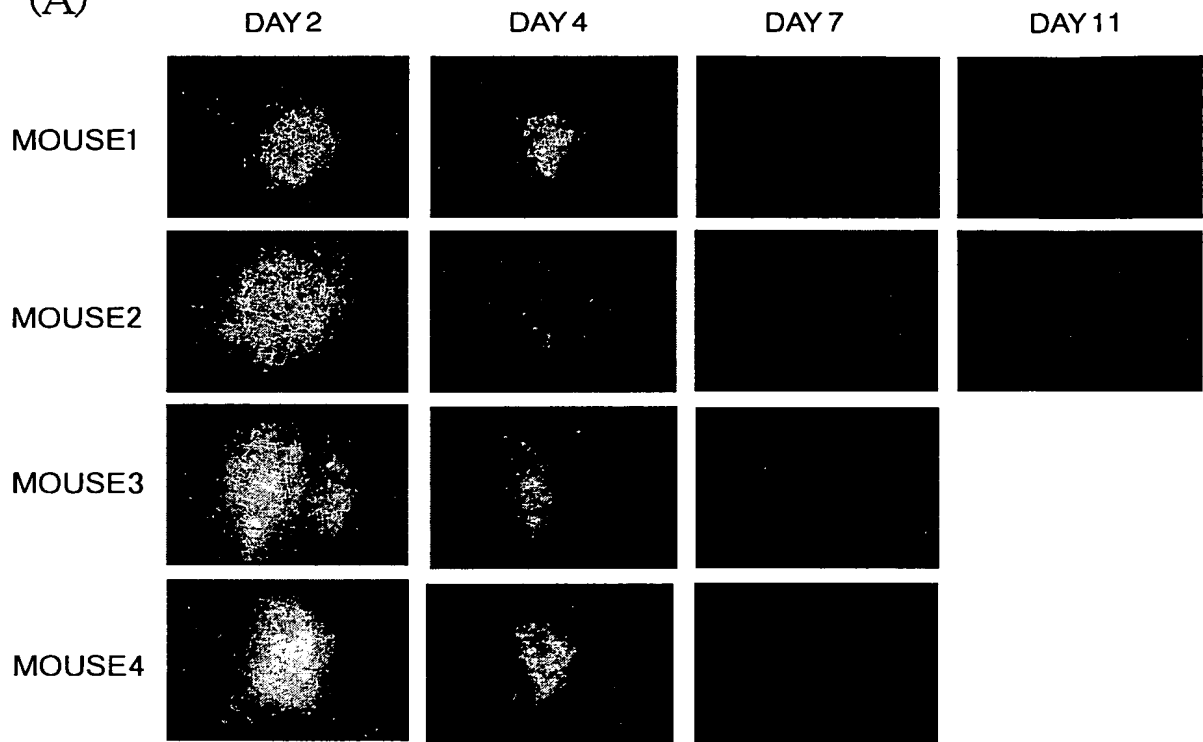


FIG. 10

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(A)



(B)

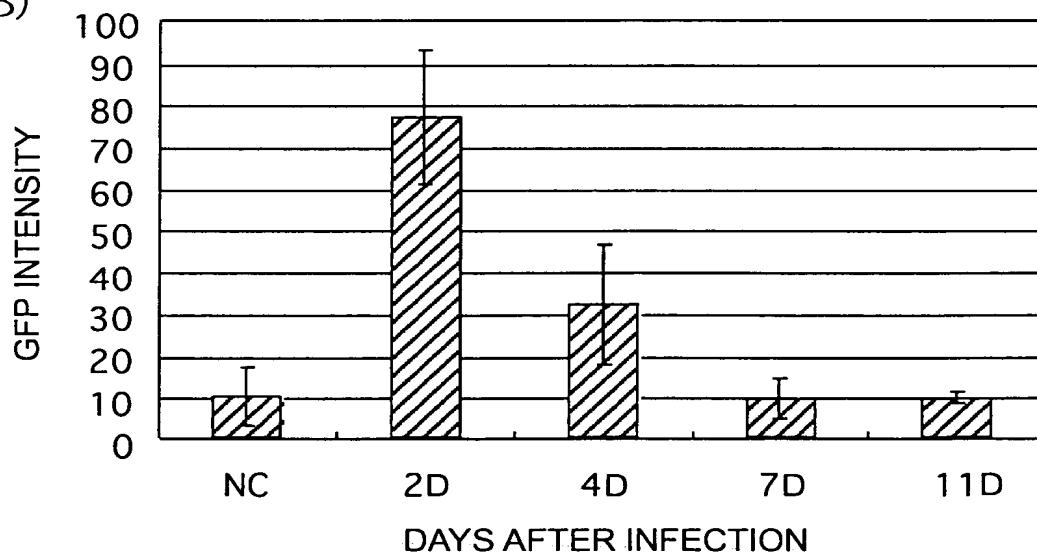


FIG. 11

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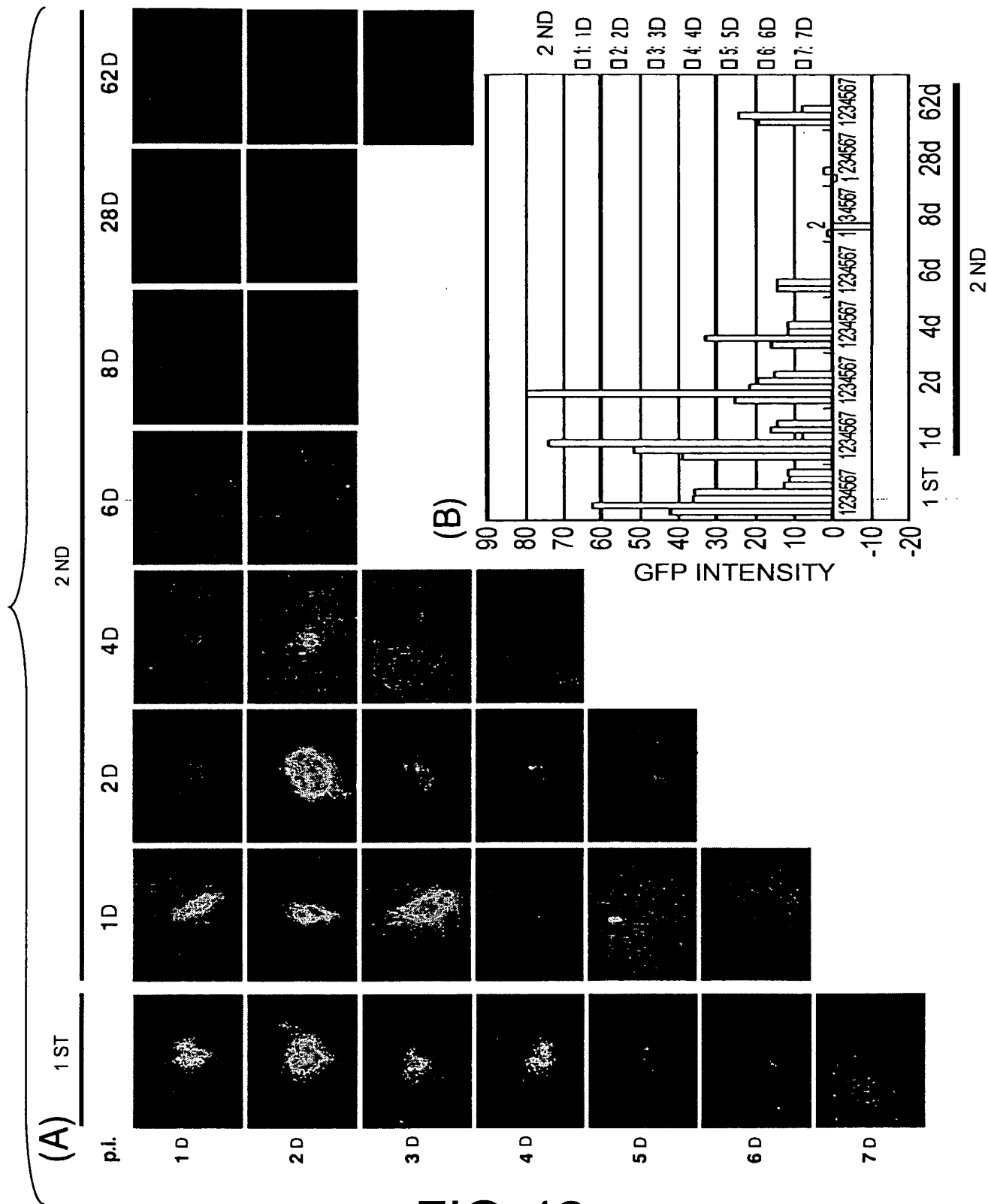


FIG. 12

(A)GFP FLUORESCENCE (B)SUPERIMPOSED (C)ANTI-GFP

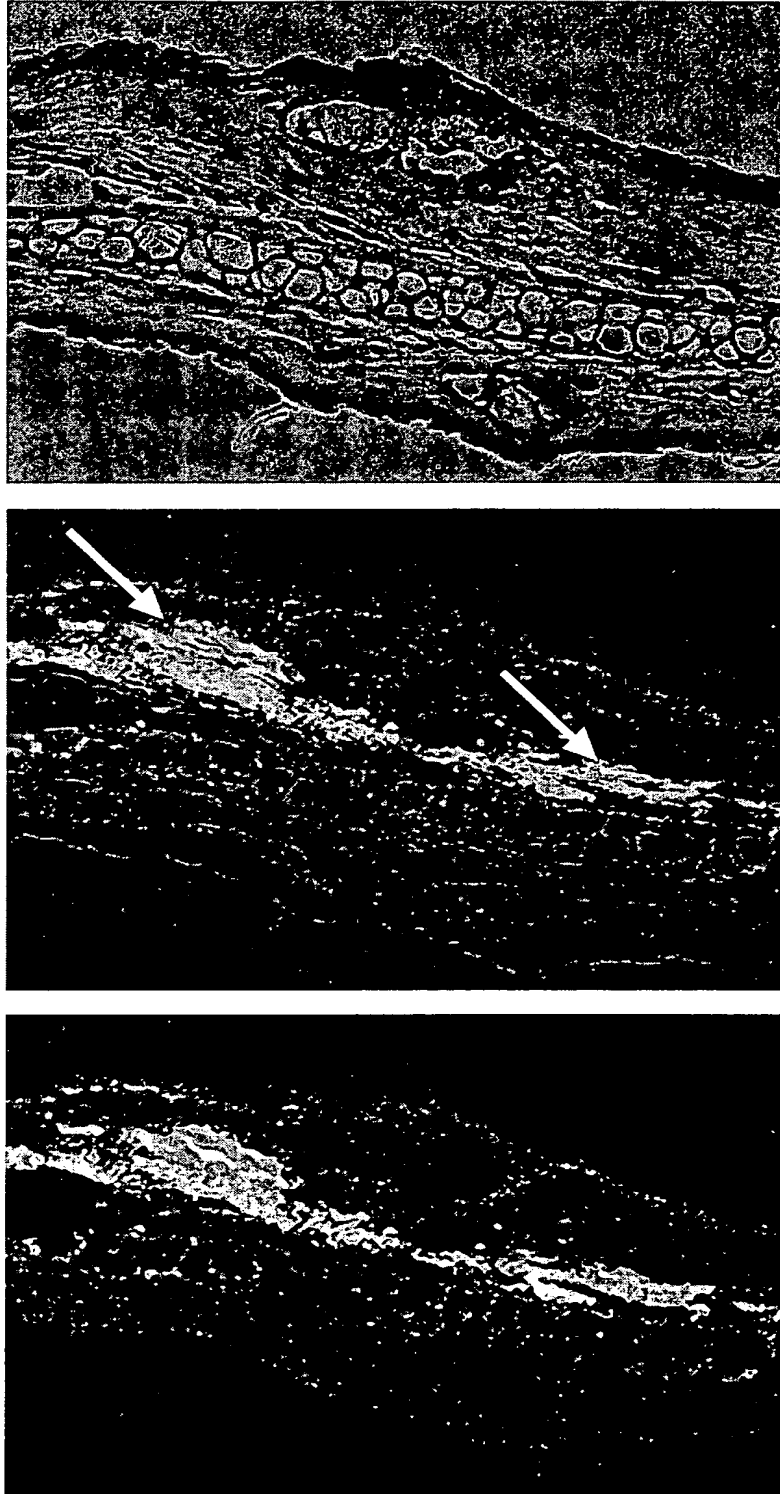


FIG. 13

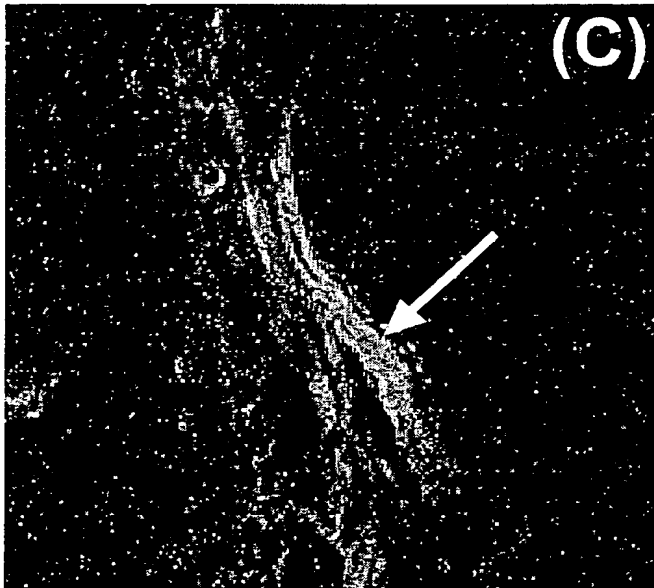
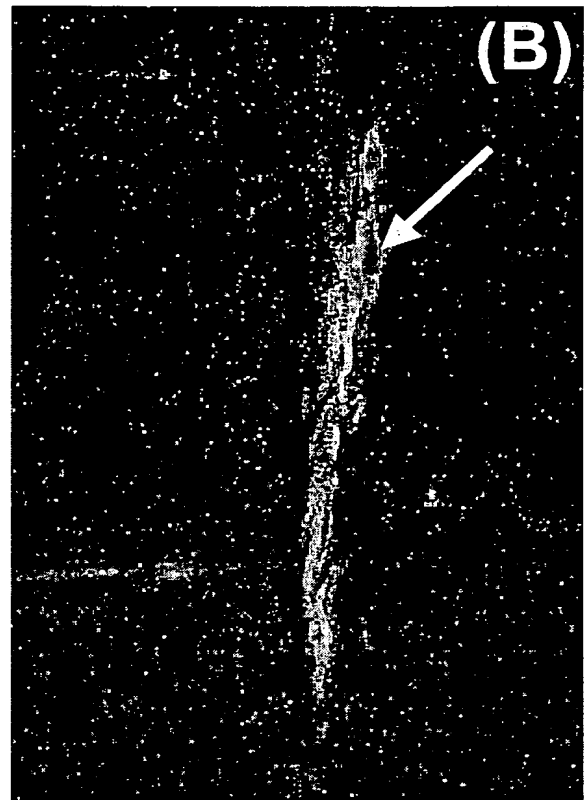
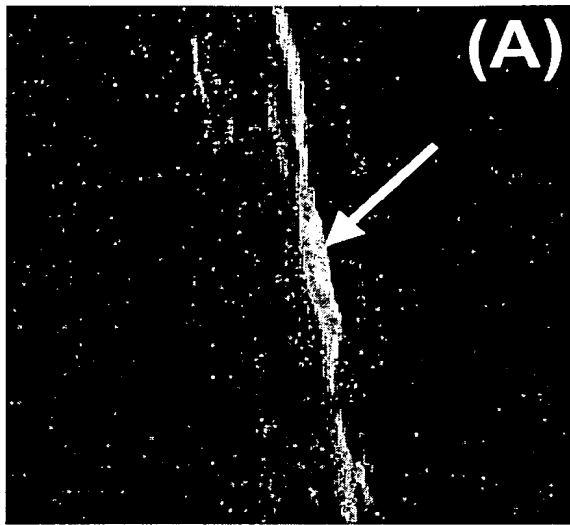
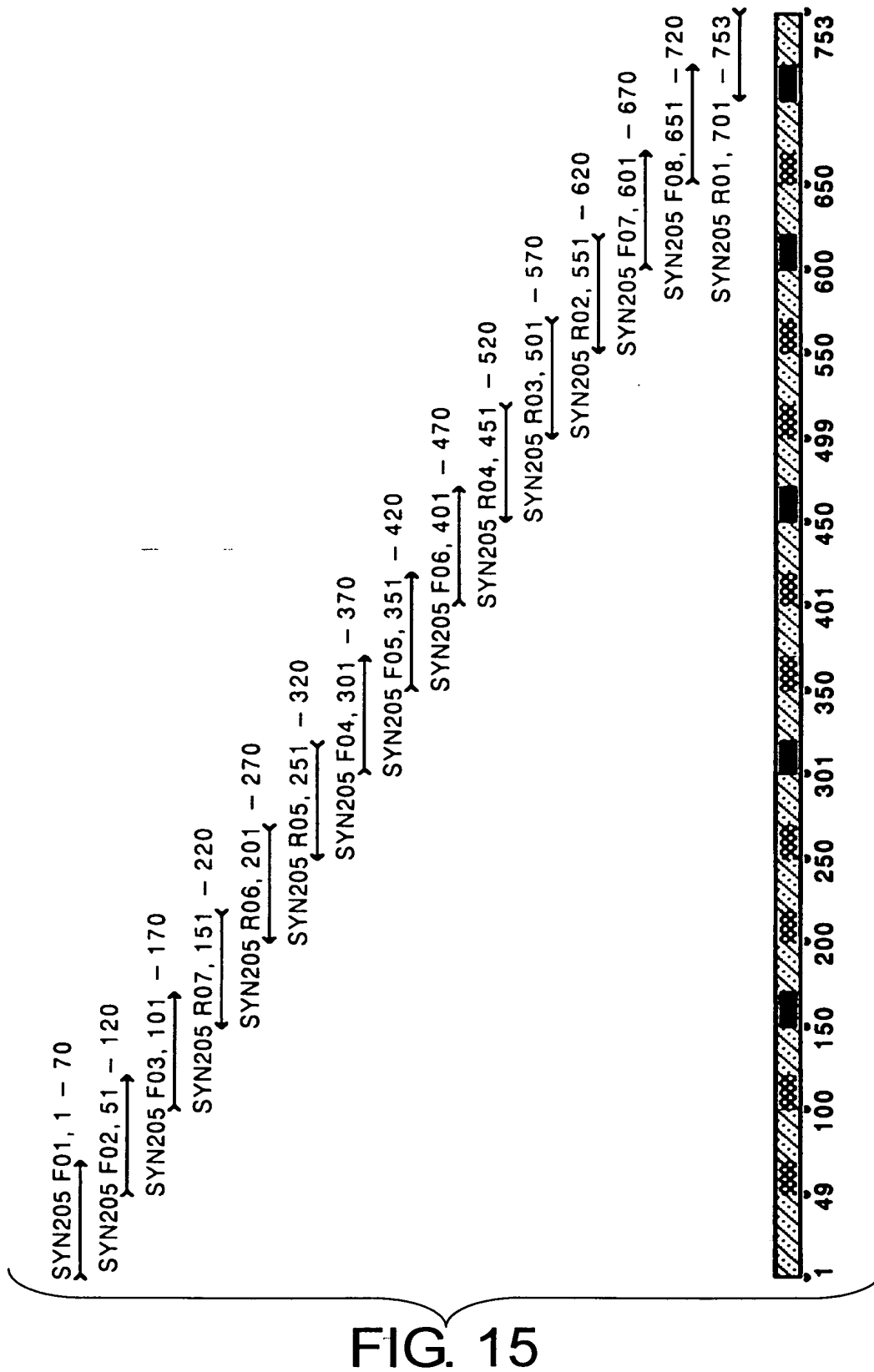


FIG. 14



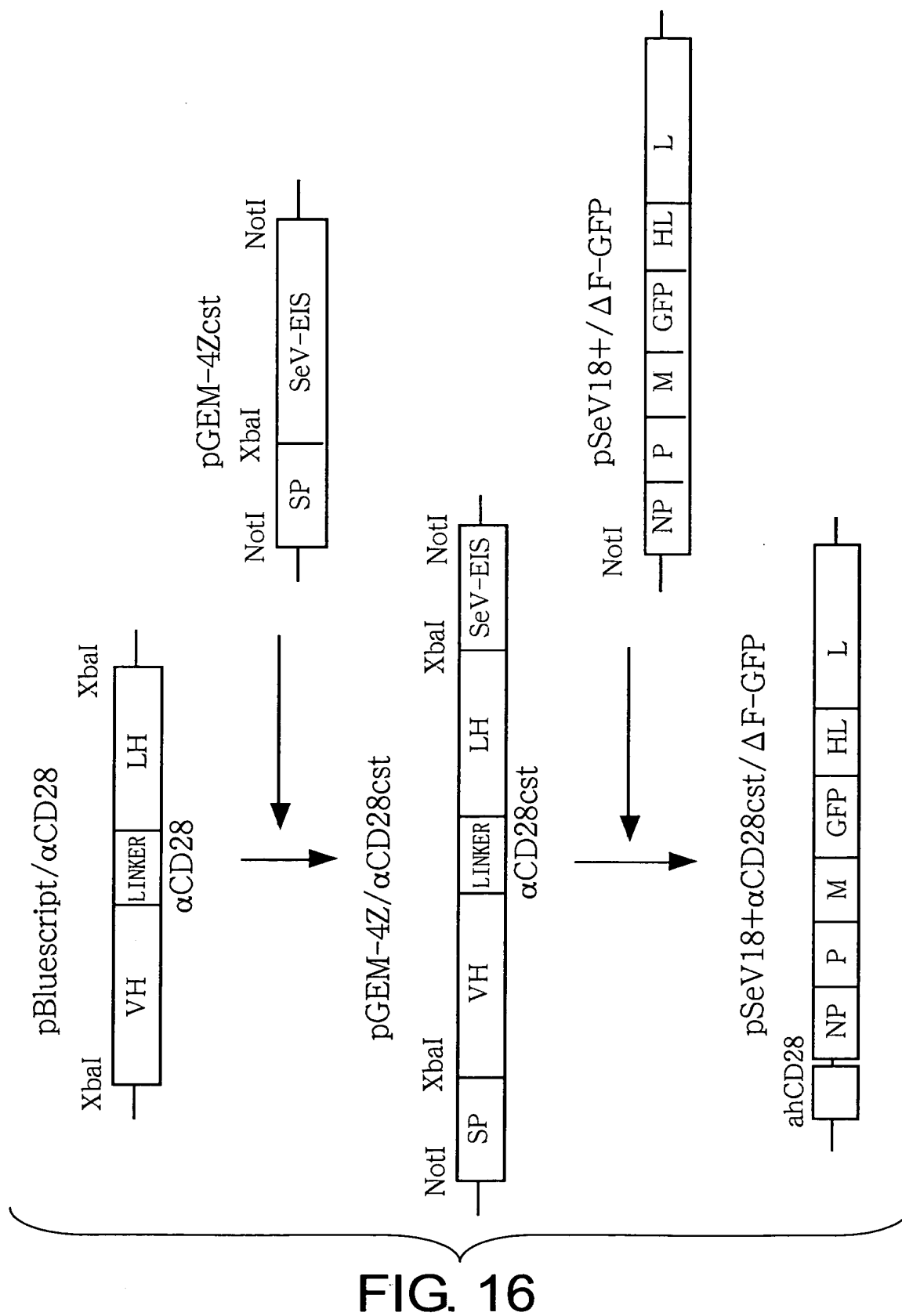
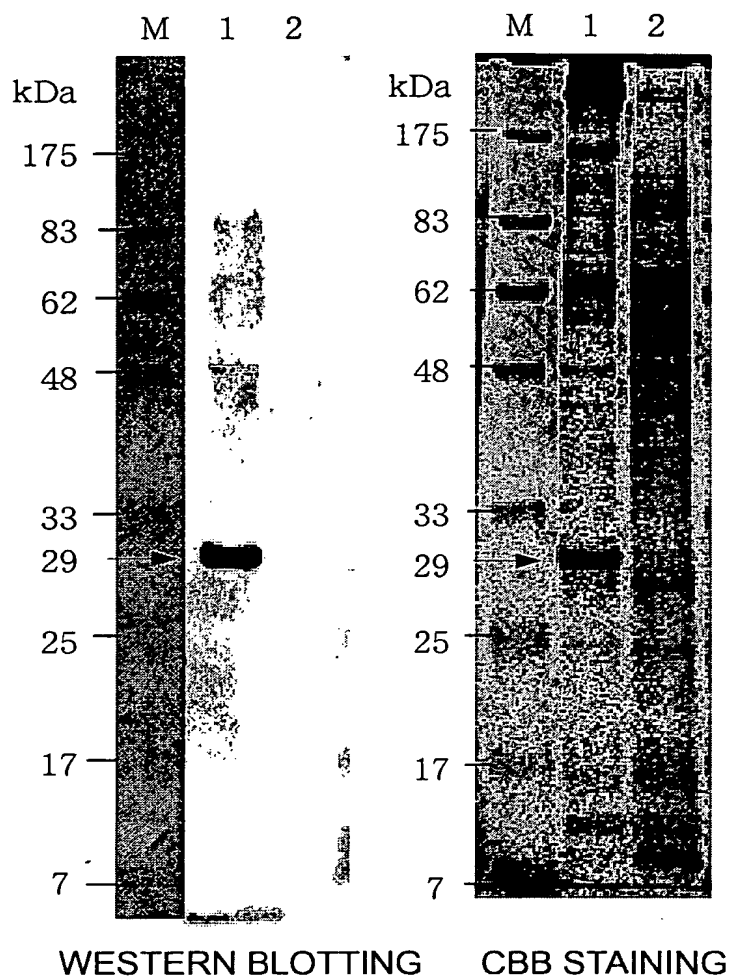




FIG. 17



M:PROTEIN MARKER

1: SeV18+ α CD28cst/ Δ F-GFP CULTURE
SUPERNATANT

2: SeV/ Δ F(GFP)CULTURE SUPERNATANT

FIG. 18

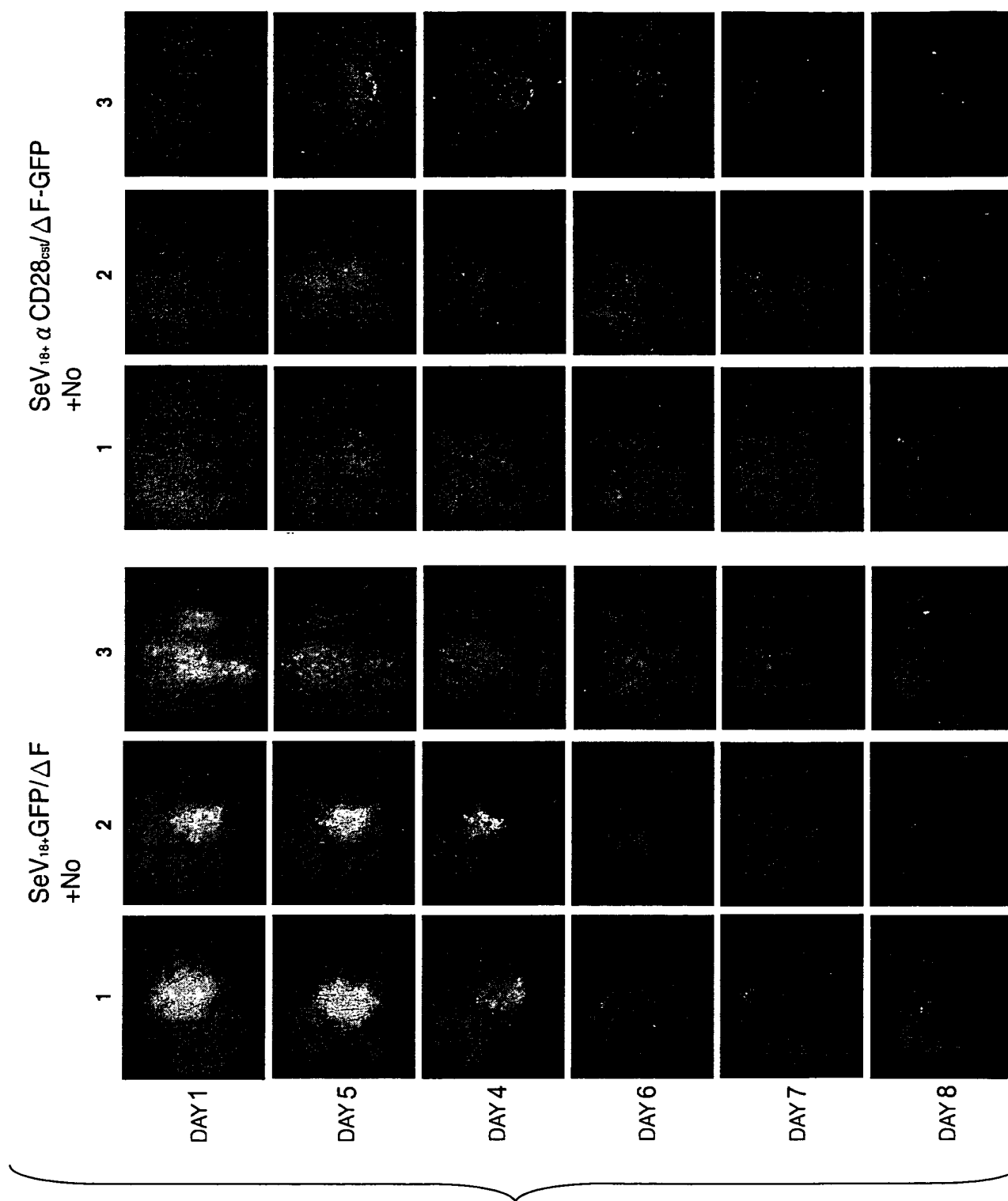


FIG. 19

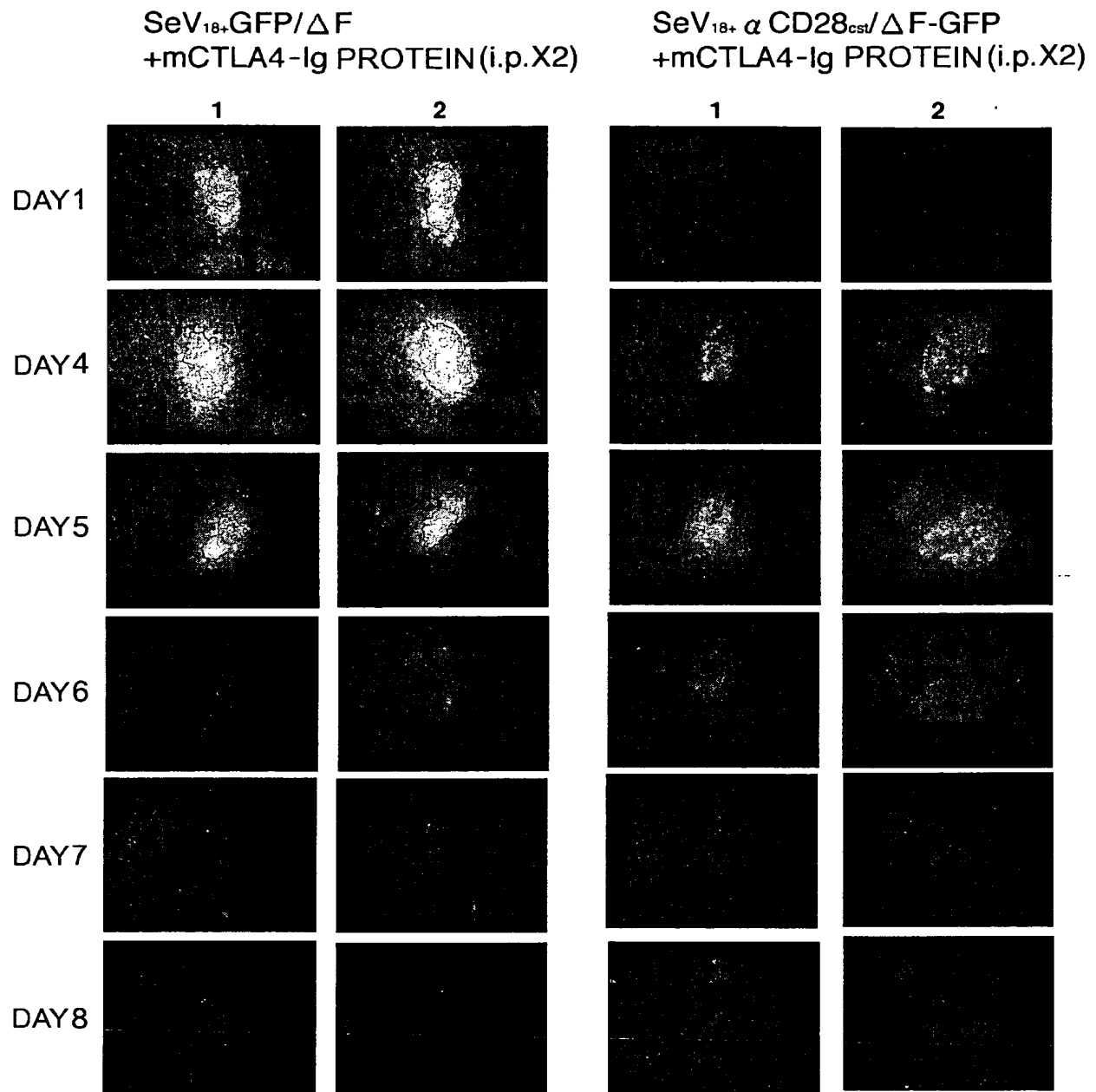


FIG. 20

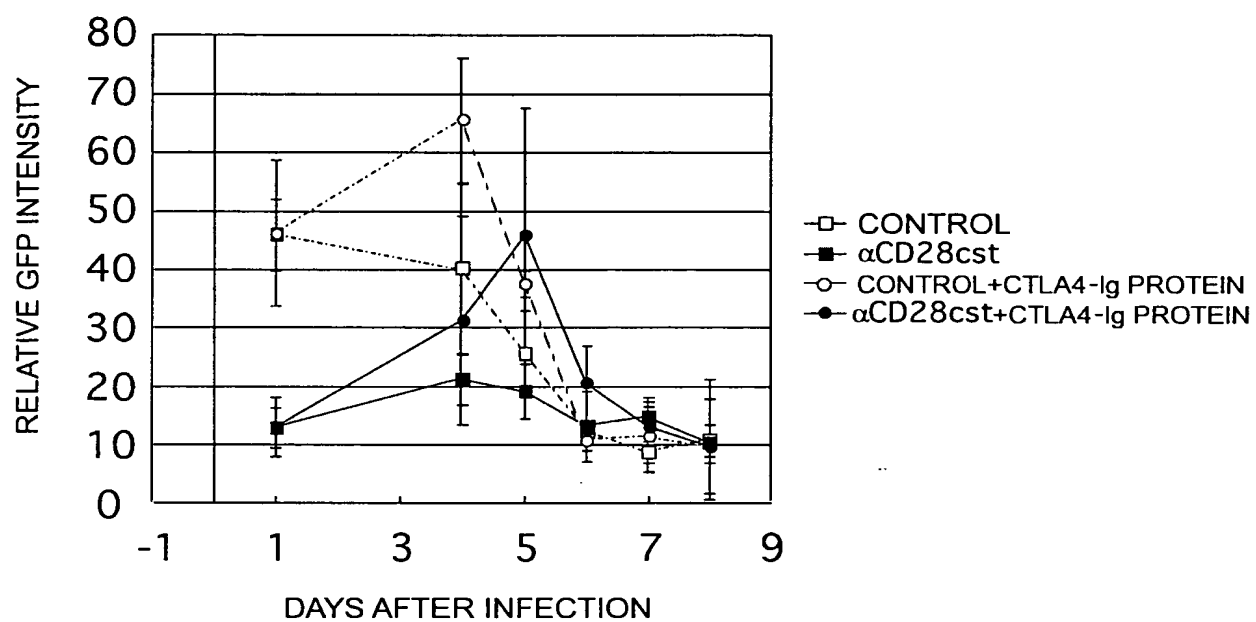


FIG. 21

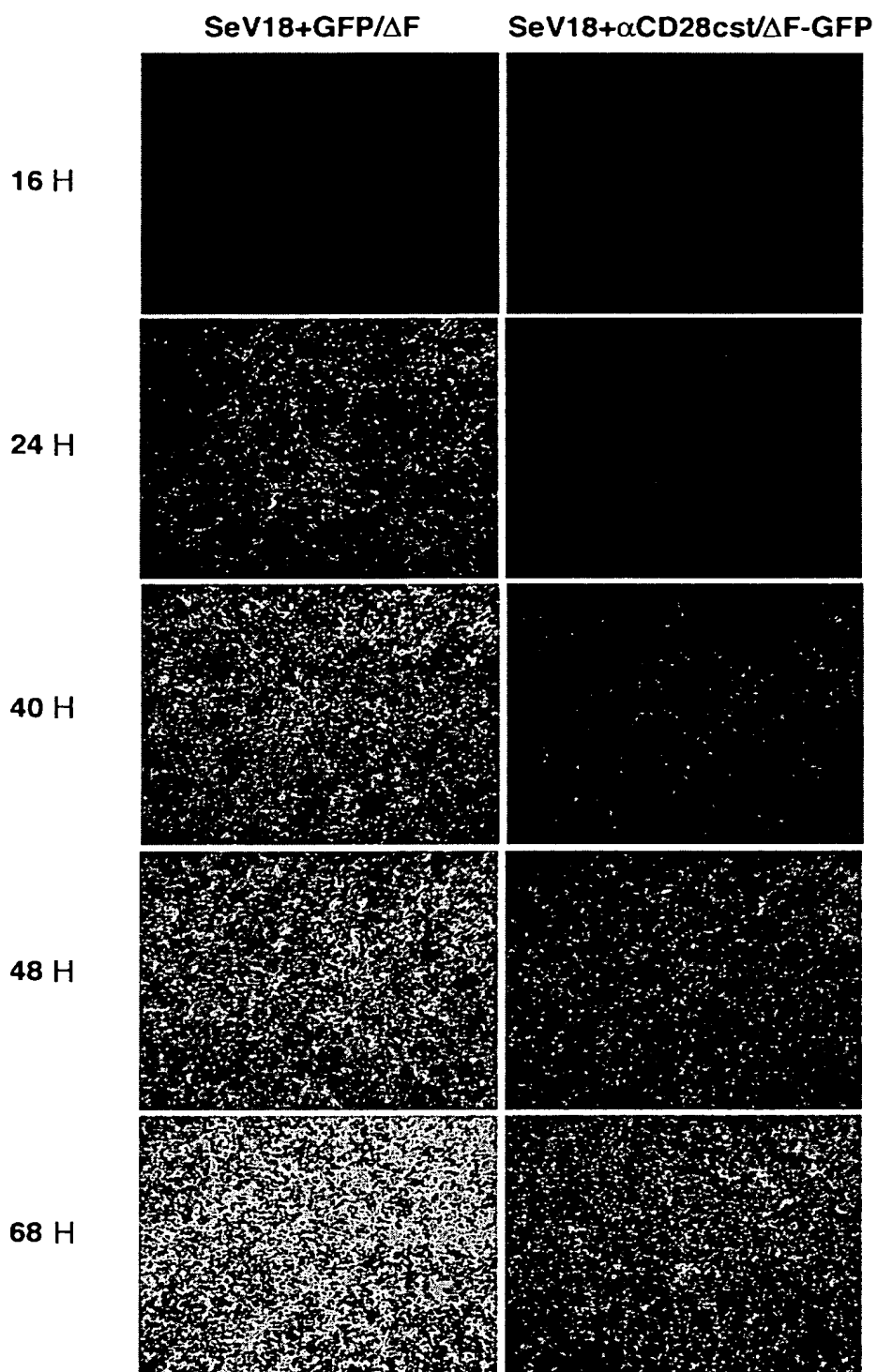


FIG. 22